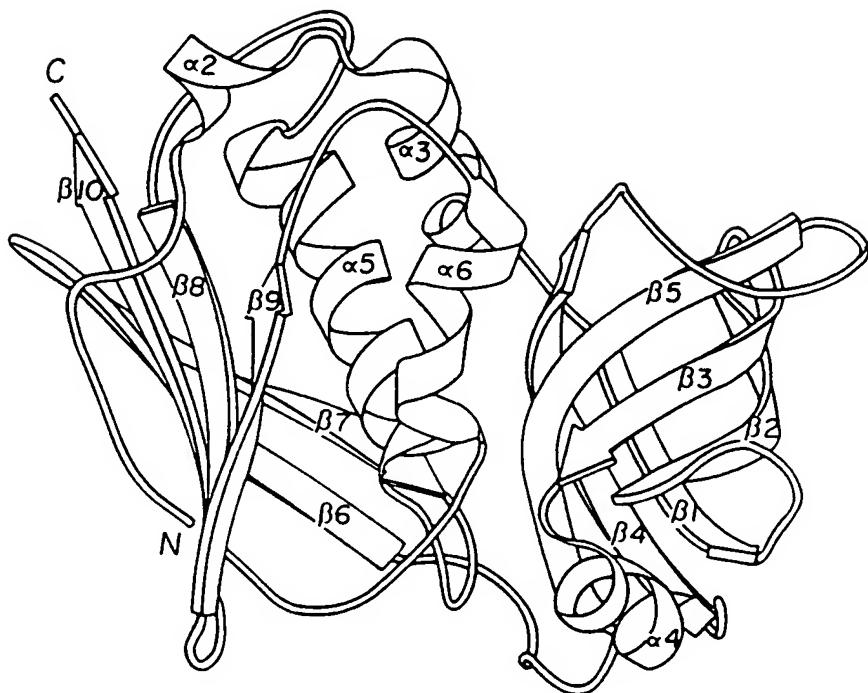


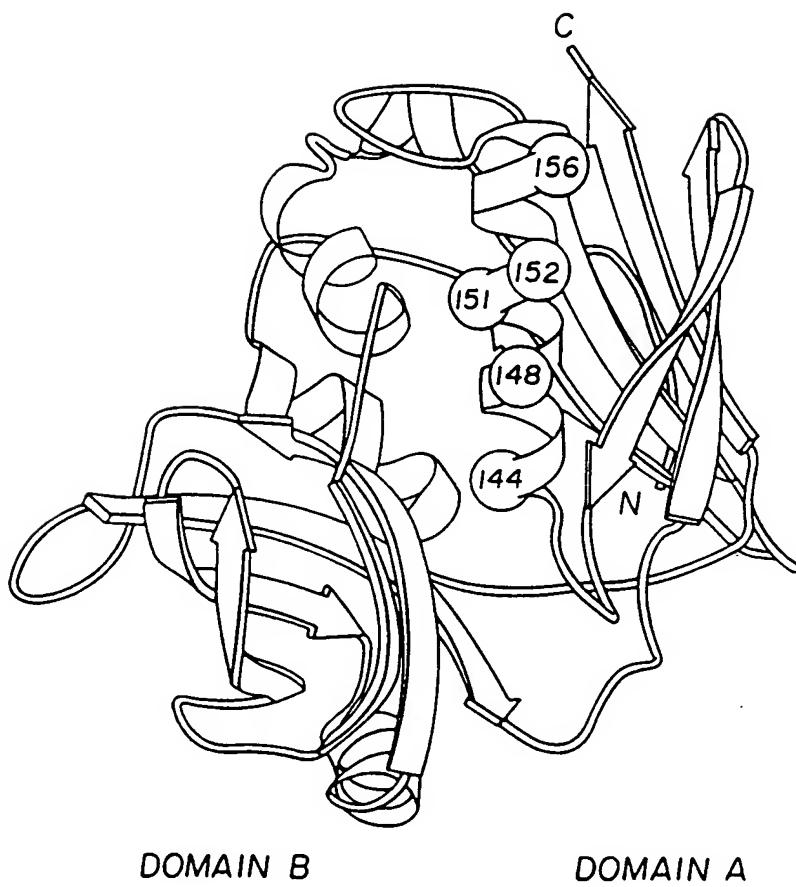
Fig. 1

DOMAIN A



DOMAIN B

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Fig. 2

DOMAIN B

DOMAIN A

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TCATGTTGACAGCTTATCATCGATAAGCTTACTTCGAATCAGGTCTATCCTGAAACAGGTGCAACATAGATTAGGCATGGAGATTTACCAAGACAA
 50 100

CTATGAACTATATACTCACATCACCGAATCGGCAATTGATGACATTGAACTAAATTCAATCAATTGTTACTAACAGCAACTAGATTGACAACAA
 150 200

TCTCAACAAACGTTAATTAAACACATTCAAGTAACCTCCACAGCTCCATCAATGCTTACCGTAAGTAATCATAACTTACTAAACCTGTTACATCAA
 250 300

GGTTTTTCTTTGCTTGTATGAGTTACCATACCTTCTATATTATTGACAACAAATTGACAACCTTCATATTATTTCTGCTACTCAAAGTT
 350 400

TTCTCATTTGATATAGTCTAATTCCACCATCACTTCTTCACTCTCACCGTCACAACTTCATCATCTCATTTCTGTTGGTAACACATAATC
 450 500

AAATATCTTCCGTTTACGCACTATCGCTACTGTGTACCTAAATATACCCCTTATCAATCGCTCTTAAACTCATCTATATAACATATTCTAT
 550 600

CCTCCTACCTATCTATTGTAAGATAAAAATAACTATTGTTTTTTGTTATTATAATAAAAATTATAAGTTAATGTTTTTAAAGAT
 650 700

ACAATTATTCTATTATAGTAGCTATTTCATTGTTAGTAATATTGGTGAATTGTAATAACCTTTAAACTAGAGGAGAACCCAGATATAAAA
 750 800

M E N N K K V L K K M V F F V L V T F L G L
 TGGAGGAATATTA ATG GAA AAC AAT AAA AAA GTA TTG AAG AAA ATG GTA TTT TTT GTT TTA GTG ACA TTT CTT GGA CTA

10
 T I S Q E V F A Q Q D P D P S Q L H R S S L V K N L
 ACA ATC TCG CAA GAG GTA TTT GCT CAA CAA GAC CCC GAT CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT

20
 Q N I Y F L Y E G D P V T H E N V K S V D Q L L S H
 CAA ATA TAT TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT GTT GAT CAA CTT TTA TCT CAC

30
 50 60 70
 D L I Y N V S G P N Y D K L K T E L K N Q E M A T L
 GAT TTA ATA TAT AAT GTT TCA GGG CCA AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT TTA

80 90
 F K D K N V D I Y G V E Y Y H L C Y L C E N A E R S
 TTT AAG GAT AAA AAC GTT GAT ATT TAT GGT GTA GAA TAT TAC CAT CTC TGT TAT TTA TGT GAA AAT GCA GAA AGG AGT

100 110 120
 A C I Y G G V T N H E G N H L E I P K K I V V K V S
 GCA TGT ATC TAC GGA GGG GTA ACA AAT CAT GAA GGG AAT CAT TTA GAA ATT CCT AAA AAG ATA GTC GTT AAA GTA TCA

130 140 150
 I D G I Q S L S F D I E T N K K M V T A Q E L D Y K
 ATC GAT GGT ATC CAA AGC CTA TCA TTT GAT ATT GAA ACA AAT AAA AAA ATG GTA ACT GCT CAA GAA TTA GAC TAT AAA

160 170 180
 V R K Y L T D N K Q L Y T N G P S K Y E T G Y I K F
 GTT AGA AAA TAT CTT ACA GAT AAT AAG CAA CTA TAT ACT AAT GGA CCT TCT AAA TAT GAA ACT GGA TAT ATA AAG TTC

190 200
 I P K N K E S F W F D F F P E P E F T Q S K Y L M I
 ATA CCT AAG AAT AAA GAA AGT TTT TCG TTT GAT TTT TTC CCT GAA CCA GAA TTT ACT CAA TCT AAA TAT CTT ATG ATA

210 220
 Y K D N E T L D S N T S Q I E V Y L T T K .
 TAT AAA GAT AAT GAA ACC CTT GAC TCA AAC ACA AGC CAA ATT GAA GTC TAC CTA ACA ACC AAG TAA CTTTTGCTTTGGC

AACCTTACCTACTGCTGATTTAGAAATTCTTATGCAATTCTTATTAAATGAAACCGCTCATTTGATGACGGTTTGTCTTATCTAAAGGAGCTTAC
 1600 1650

CTCTTAATGCTOCAAAATTAAATCTTOGATTTGTATTTGTATTTGATGGTAATCCCATTCTGACAGACATGTCGCCACCTCTAACAA
 1700 1750

CCAAAATCATAGACAGGAGCTTGTAGCTTAGCAACTATTTATCGTC 3.
 1800 1837

FIG. 3
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Fig. 4b

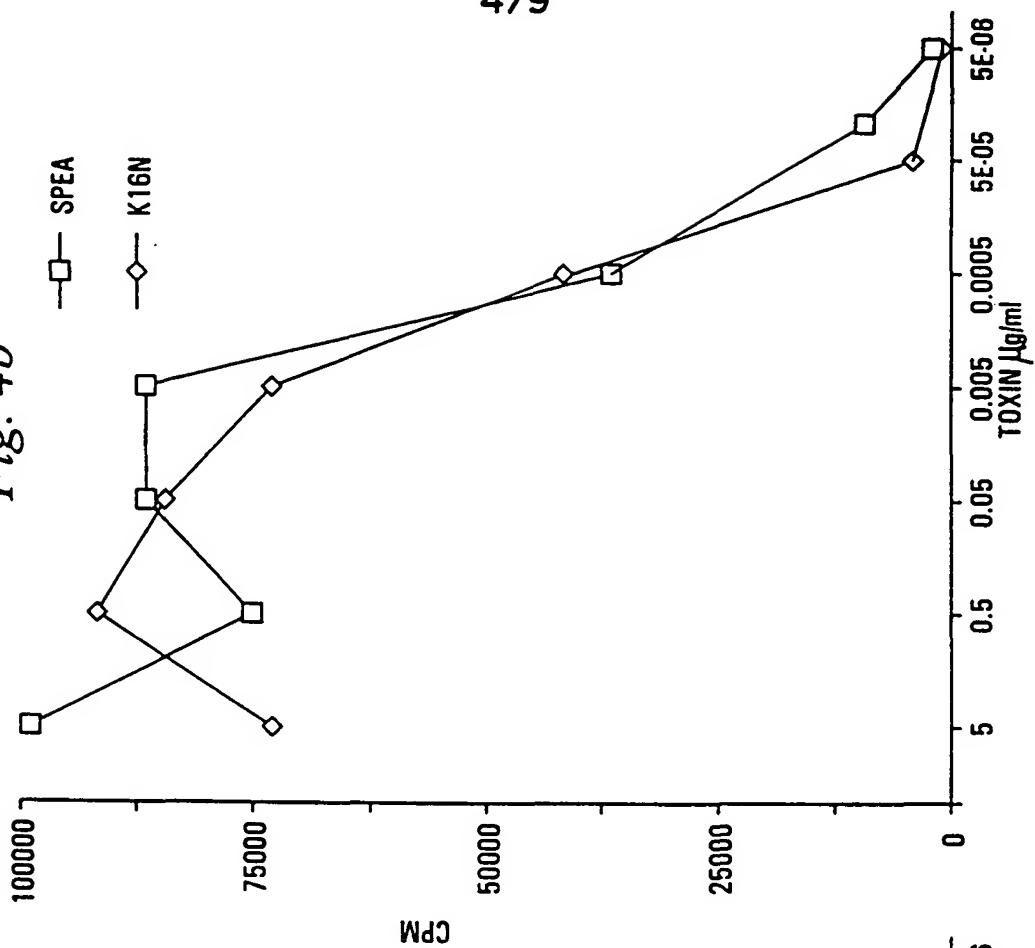
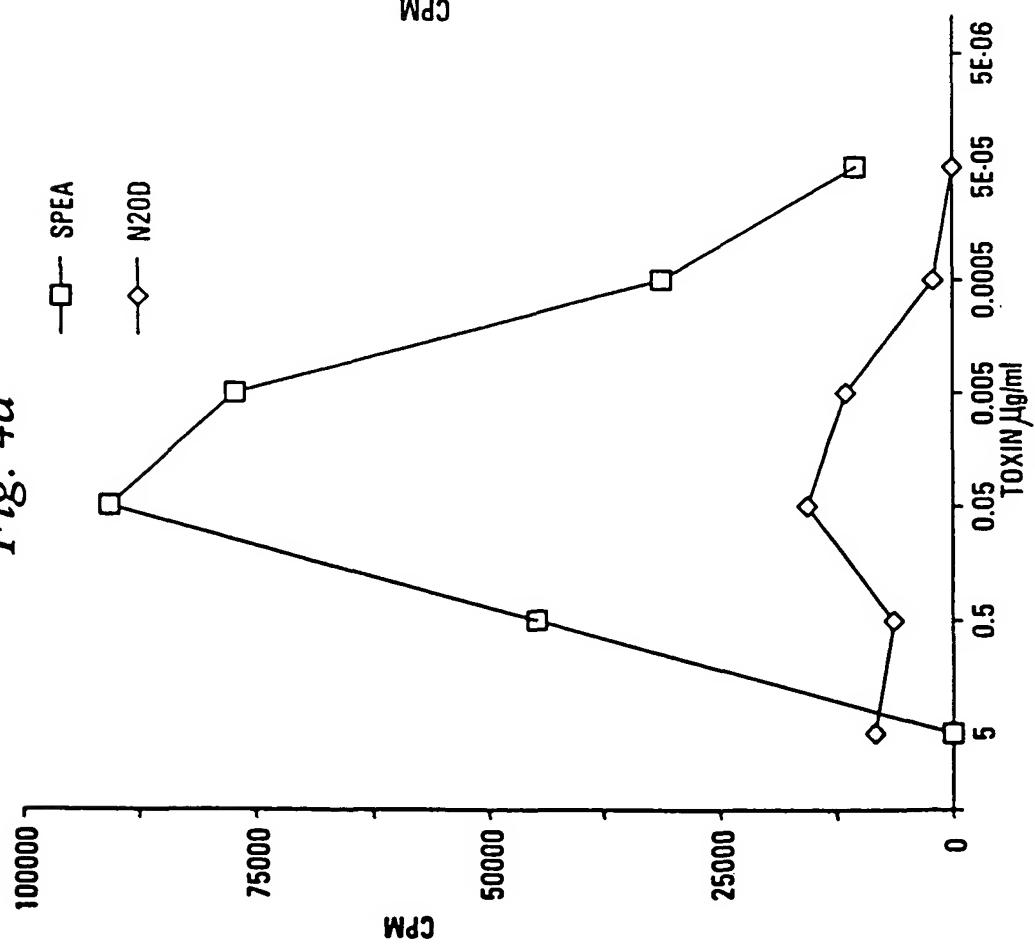
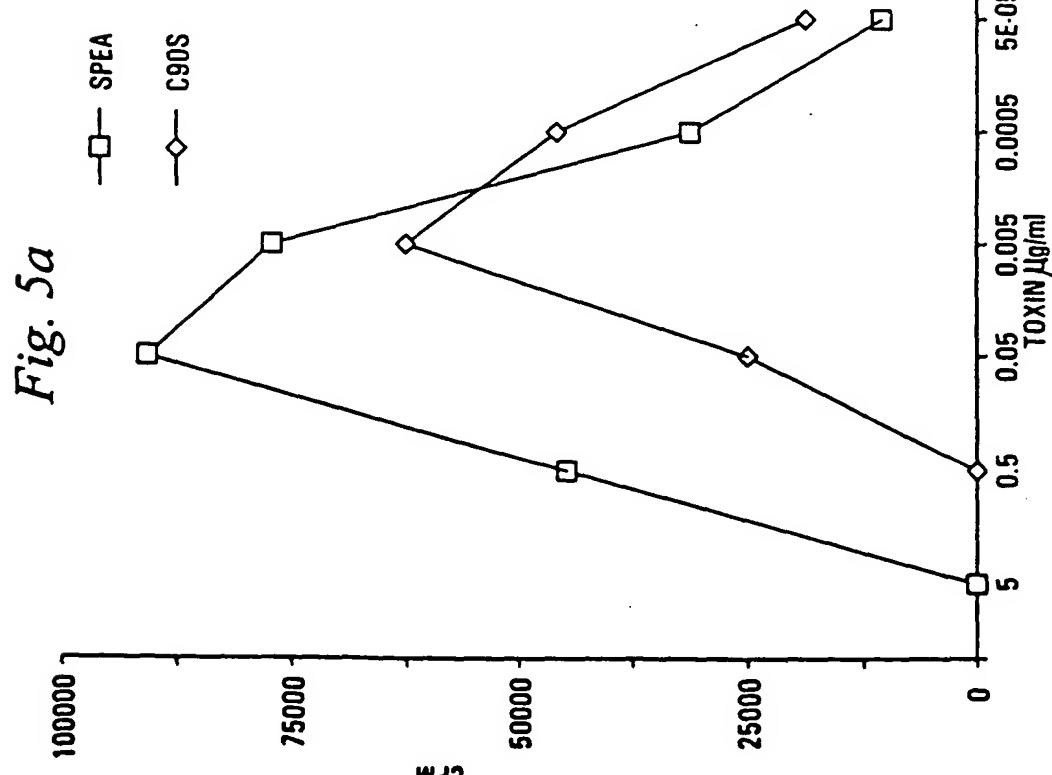
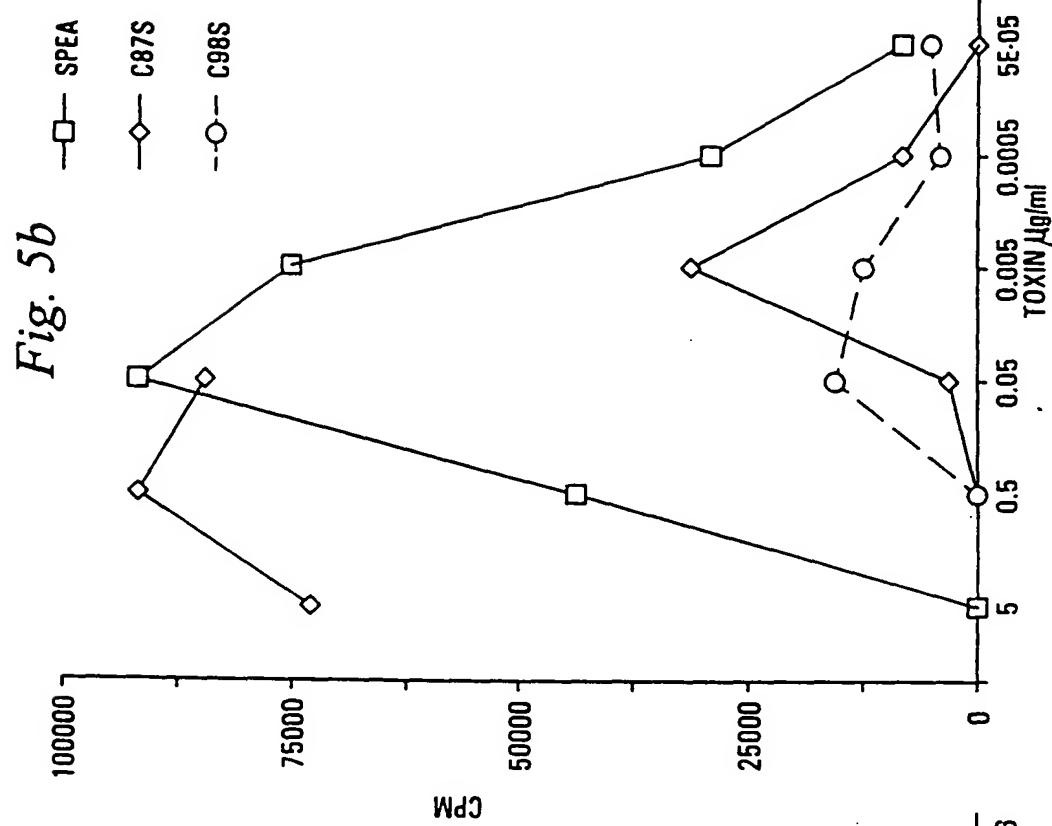


Fig. 4a



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Fig. 6b

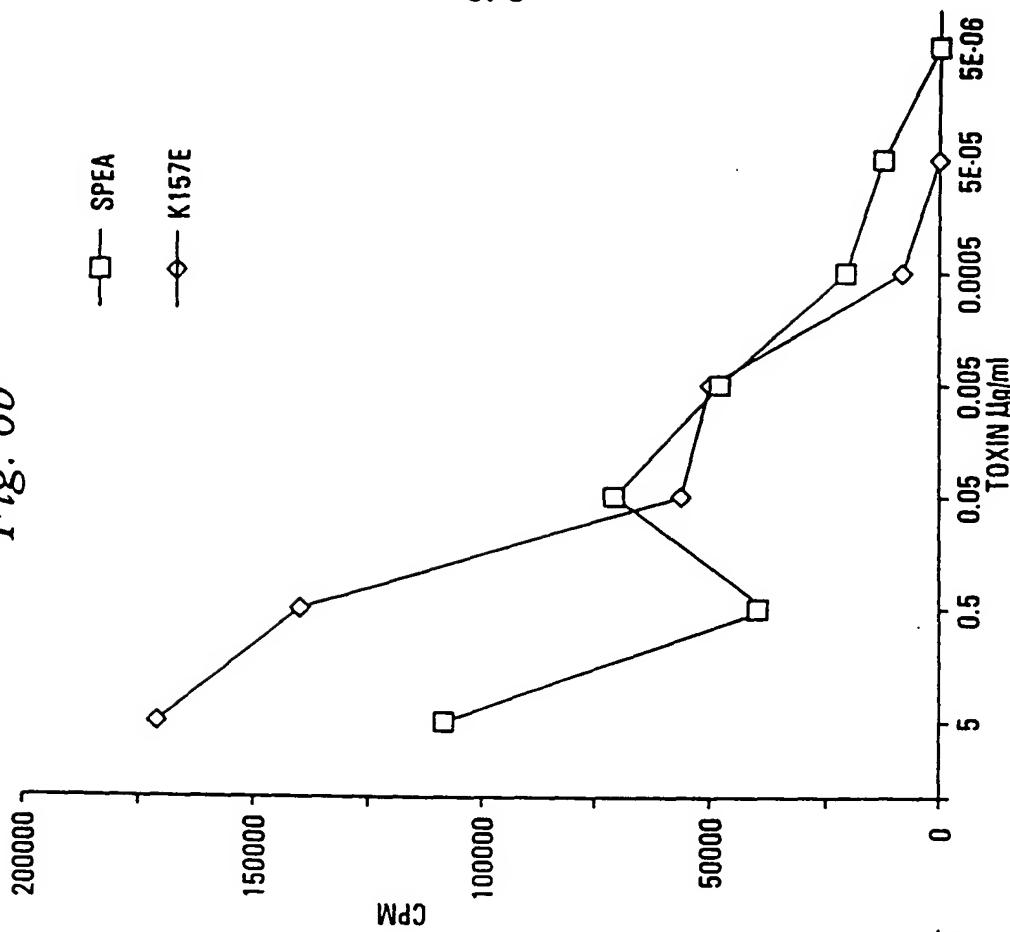
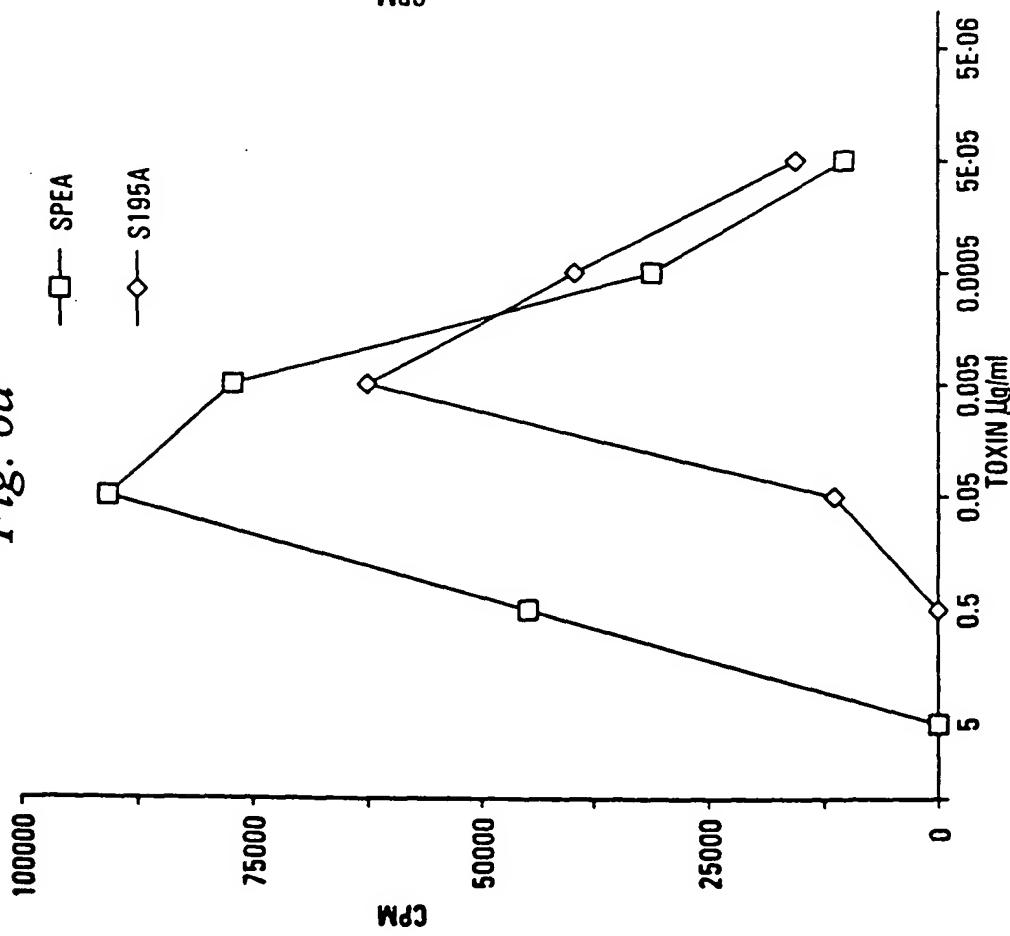
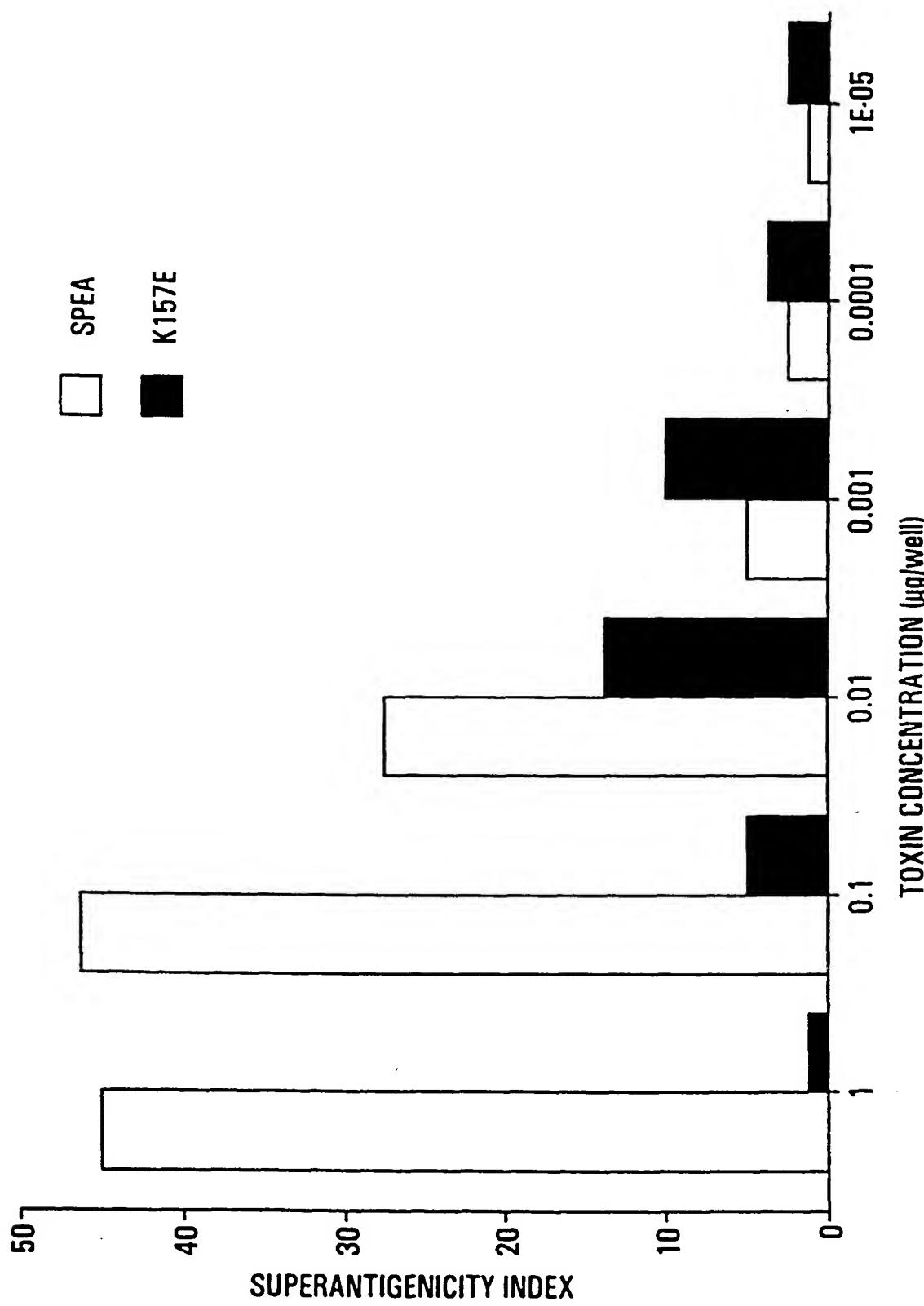


Fig. 6a

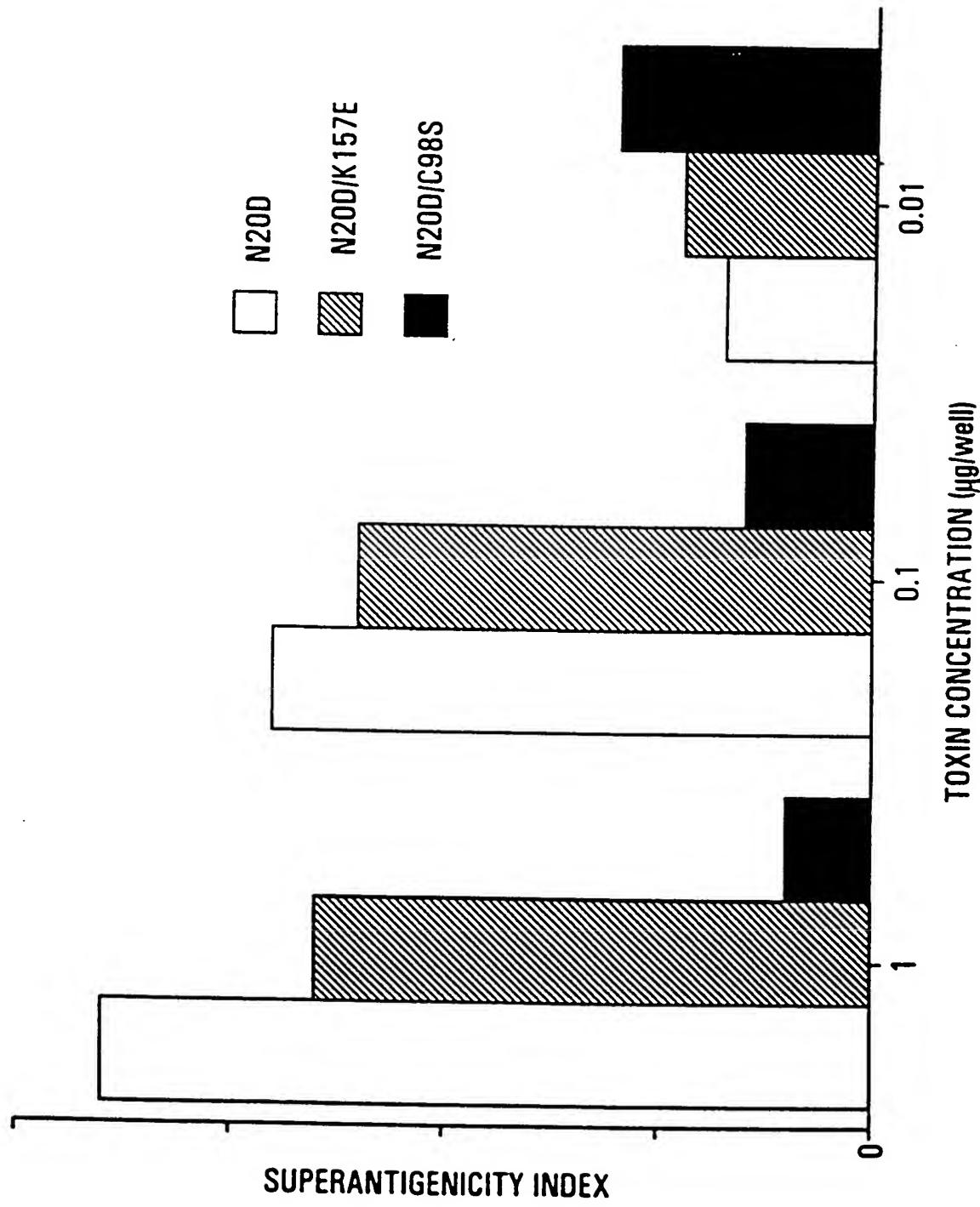


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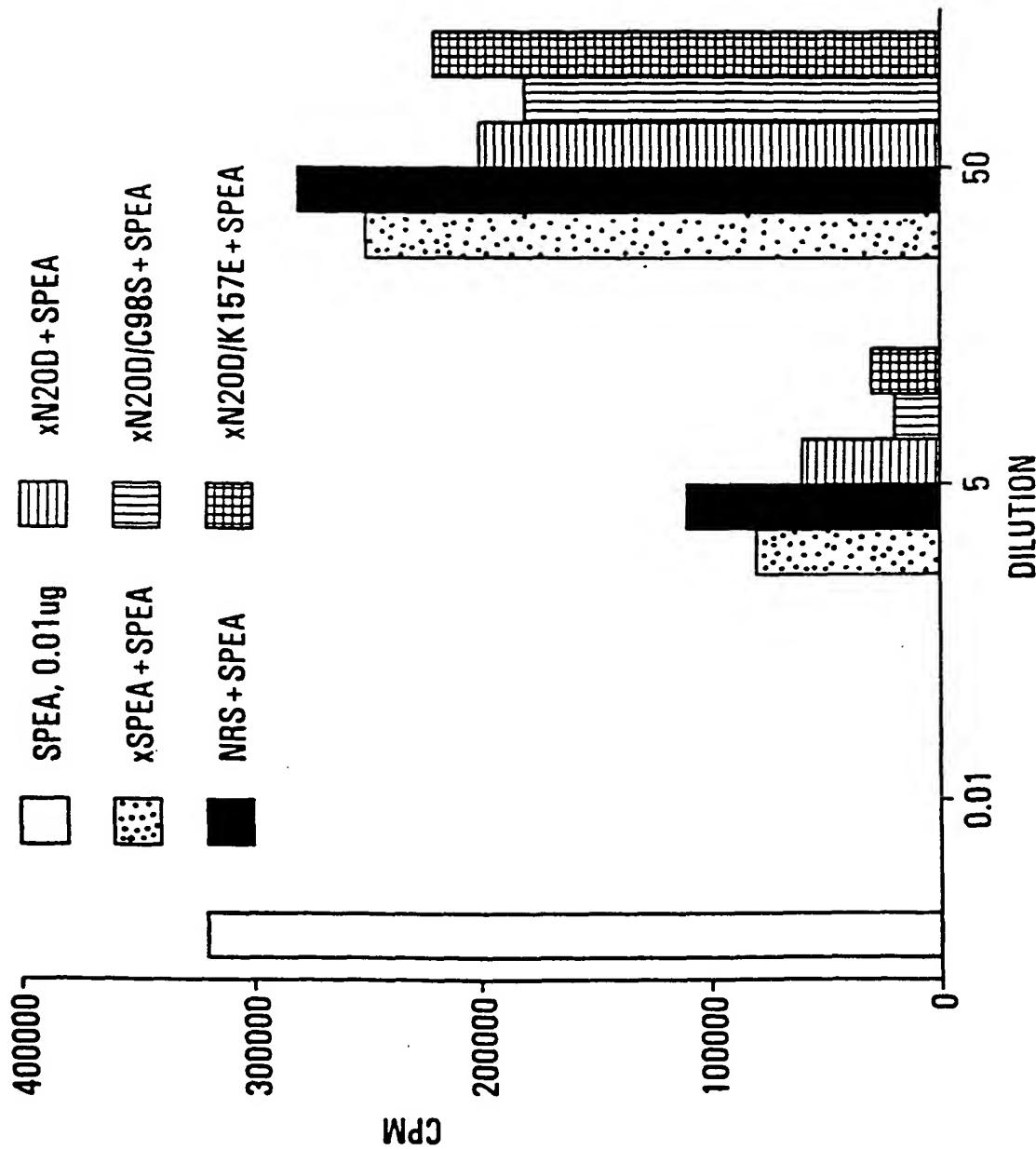
Fig. 7



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Fig. 8

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Fig. 9**SUBSTITUTE SHEET (RULE 26)**